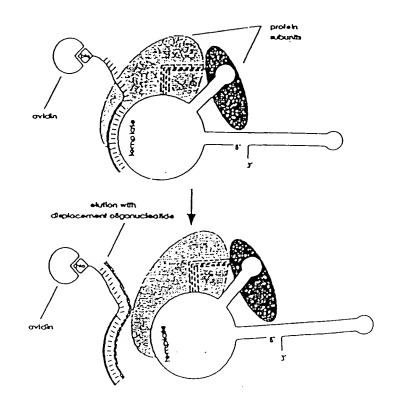
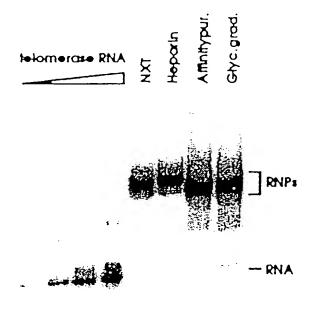
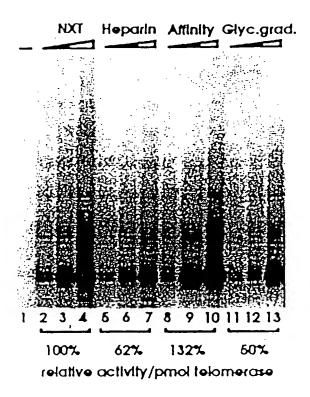
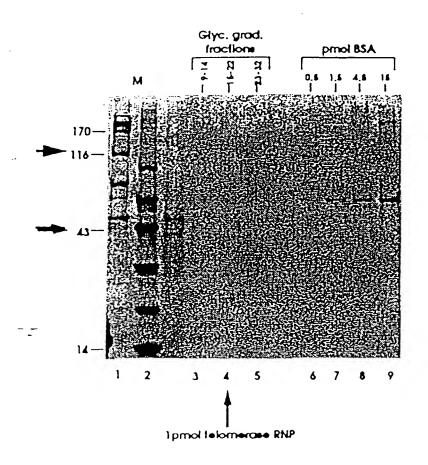
PANEL A

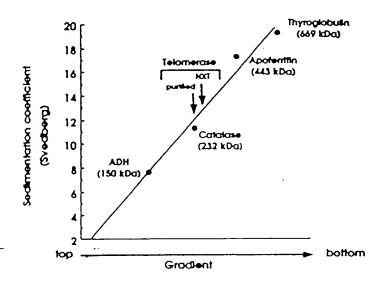
PANEL B

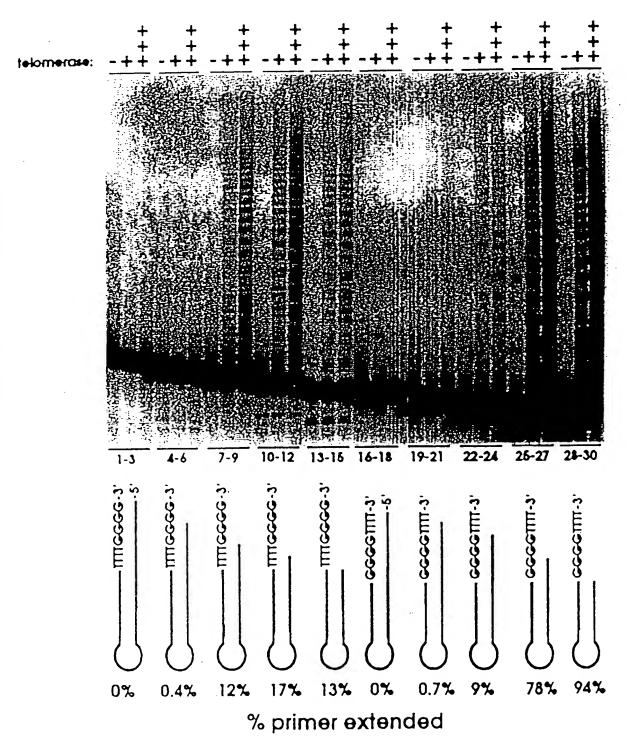


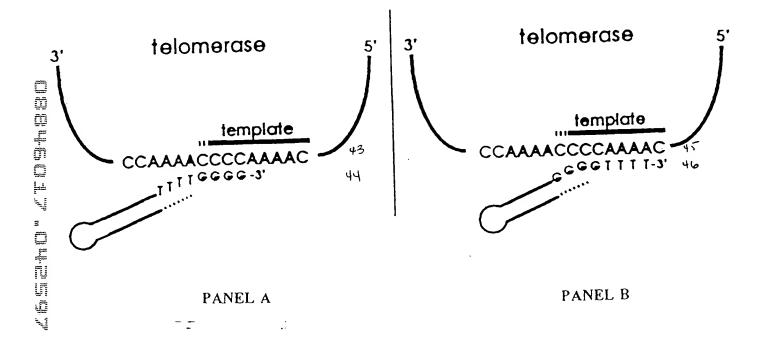


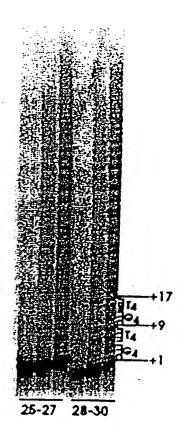












1 AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT 51 AACCTCAGTA TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA 101 ATGGAGGTTG ATGTTGATAA TCAAGCTGAT AATCATGGCA TTCACTCAGC 151 TCTTAAGACT TGTGAAGAAA TTAAAGAAGC TAAAACGTTG TACTCTTGGA 201 TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA TTATAAAGAT 251 TTAGAAGATA TTAAAATATT TGCGCAGACA AATATTGTTG CTACTCCACG 301 AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT 351 CAACTGGACT AATGATCGAA CTTATTGACA AATGCTTAGT TGAACTTCTT 401 TCATCAAGCG ATGTTTCAGA TAGACAAAAA CTTCAATGAT TTGGATTTCA 451 ACTTAAGGGA AATCAATTAG CAAAGACCCA TTTATTAACA GCTCTTTCAA 501 CTCAAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT TAGAGCAATG 551 ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA 601 GCGAACTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG 651 ATCATTTGAA AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA 701 GCAGACATGA ATGAACCTCG ATGTTGATCA ACCTGCAAAT ACAATGTCAA 751 GAATGAGAAA GATCACTTTC TCAACAACAT CAACGTGCCG AATTGGAATA 801 ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT TAATAGAAAT 851 AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTC 901 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA 951 GAATTAGAAA GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG 1001 CTTGAGAAAG TCAAAGATTT TAACTTCAAC TACTATTTAA CAAAATCTTG 1051 TCCTCTTCCA GAAAATTGGC GGGAACGGAA ACAAAAAATC GAAAACTTGA 1101 TAAATAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA GCTGTTTAGC 1151 TACACAACTG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTTCTA 1201 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC 1251 AAAAGAAAGT TAAGAAATAT GTGGAACTAA ACAAGCATGA ACTCATTCAC 1301 AAAAACTTAT TGCTTGAGAA GATCAATACA AGAGAAATAT CATGGATGCA 1351 GGTTGAGACC TCTGCAAAGC ATTTTTATTA TTTTGATCAC GAAAACATCT 1401 ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT CGTCGTCTCG 1451 CTGATTAGAT GATTTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA 1501 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA 1551 TCGCAGACTT AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT 1601 GAAGAATGGA AAAAGTCGCT TGGATTTGCA CCTGGAAAAC TCAGACTAAT 1651 ACCGAAGAAA ACTACTTTCC GTCCAATTAT GACTTTCAAT AAGAAGATTG 1701 TAAATTCAGA CCGGAAGACT ACAAAATTAA CTACAAATAC GAAGTTATTG 1751 AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC 1801 TTTTGGATTC GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG 1851 AGTTTGTTTG CAAATGGAAG CAAGTTGGAC AACCAAAACT CTTCTTTGCA 1901 ACTATGGATA TCGAAAAGTG ATATGATAGT GTAAACAGAG AAAAACTATC 1951 AACATTCCTA AAAACTACTA AATTACTTC TTCAGATTTC TGGATTATGA 2001 CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA TTCGAAAAAC 2051 TTTAGAAAGA AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT 2101 TGCACTTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTTGAAAATG 2201 AGAAATTATT TTAAGAAAGA TAACTTACTT CAACCAGTCA TTAATATTTG 2251 CCAATATAAT TACATTAACT TTAATGGGAA GTTTTATAAA CAAACAAAAG 2301 GAATTCCTCA AGGTCTTTGA GTTTCATCAA TTTTGTCATC ATTTTATTAT

FIGURE 9 (cont.)

2351	GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA
2401	CCCTGAAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC
2451	TTTTGATTAC AACTCAAGAG AATAATGCAG TATTGTTTAT TGAGAAACTT
2501	ATAAACGTAA GTCGTGAAAA TGGATTTAAA TTCAATATGA AGAAACTACA
2551	GACTAGTTTT CCATTAAGTC CAAGCAAATT TGCAAAATAC GGAATGGATA
2601	GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG GATTGGCATC
2651	TCAATTGATA TGAAAACTCT TGCTTTAATG CCAAATATTA ACTTGAGAAT
2701	AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT
2751	CAATGTGGCT CAAGAAGAAA CTAAAGTCGT TTTTAATGAA TAACATTACC
2801	CATTATTTTA GAAAGACGAT TACAACCGAA GACTTTGCGA ATAAAACTCT
2851	CAACAAGTTA TTTATATCAG GCGGTTACAA ATACATGCAA TGAGCCAAAG
2901	AATACAAGGA CCACTTTAAG AAGAACTTAG CTATGAGCAG TATGATCGAC
2951	TTAGAGGTAT CTAAAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA
3001	CCTTGTGTGC AATATTAAGG ATACAATTTT TGGAGAGGAG CATTATCCAG
3051	ACTTTTCCT TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAA
3101	AAGTACATTT TCAACAGAGT TTGCATGATC CTCAAGGCAA AAGAAGCAAA
3151	GCTAAAAAGT GACCAATGTC AATCTCTAAT TCAATATGAT GCATAGTCGA
3201	CTATTCTAAC TTATTTTGGA AAGTTAATTT TCAATTTTTG TCTTATATAC

3251 TGGGGTTTTG GGGTTTTGGG GTTTTGGGG

- 1 MEVDVDNQAD NHGIHSALKT CEEIKEAKTL YSWIQKVIRC RNQSQSHYKD
- 51 LEDIKIFAOT NIVATPRDYN EEDFKVIARK EVFSTGLMIE LIDKCLVELL
- 101 SSSDVSDRQK LQCFGFQLKG NQLAKTHLLT ALSTQKQYFF QDEWNQVRAM
- 151 IGNELFRHLY TKYLIFQRTS EGTLVQFCGN NVFDHLKVND KFDKKQKGGA
- 201 ADMNEPRCCS TCKYNVKNEK DHFLNNINVP NWNNMKSRTR IFYCTHFNRN
- 251 NOFFKKHEFV SNKNNISAMD RAQTIFTNIF RFNRIRKKLK DKVIEKIAYM
- 301 LEKVKDFNFN YYLTKSCPLP ENWRERKQKI ENLINKTREE KSKYYEELFS
- 351 YTTDNKCVTQ FINEFFYNIL PKDFLTGRNR KNFQKKVKKY VELNKHELIH
- 401 KNLLLEKINT REISWMQVET SAKHFYYFDH ENIYVLWKLL RWIFEDLVVS
- 451 LIRCFFYVTE QQKSYSKTYY YRKNIWDVIM KMSIADLKKE TLAEVQEKEV
- 501 EEWKKSLGFA PGKLRLIPKK TTFRPIMTFN KKIVNSDRKT TKLTTNTKLL
- 551 NSHLMLKTLK NRMFKDPFGF AVFNYDDVMK KYEEFVCKWK QVGQPKLFFA
- 601 TMDIEKCYDS VNREKLSTFL KTTKLLSSDF WIMTAQILKR KNNIVIDSKN
- 651 FRKKEMKDYF RQKFQKIALE GGQYPTLFSV LENEQNDLNA KKTLIVEAKQ
- 701 RNYFKKDNLL QPVINICQYN YINFNGKFYK QTKGIPQGLC VSSILSSFYY
- 751 ATLEESSLGF LRDESMNPEN PNVNLLMRLT DDYLLITTQE NNAVLFIEKL
- 801 INVSRENGFK FNMKKLQTSF PLSPSKFAKY GMDSVEEQNI VQDYCDWIGI
- 851 SIDMKTLALM PNINLRIEGI LCTLNLNMQT KKASMWLKKK LKSFLMNNIT
- 901 HYFRKTITTE DFANKTLNKL FISGGYKYMQ CAKEYKDHFK KNLAMSSMID
- 951 LEVSKIIYSV TRAFFKYLVC NIKDTIFGEE HYPDFFLSTL KHFIEIFSTK
- 1001 KYIFNRVCMI LKAKEAKLKS DQCQSLIQYD A

1751 GGGGTTTTGG GG

1	CCCCAAAACC CCAAAACCCC AAAACCCCTA TAAAAAAAGA AAAAATTGAG
51	GTAGTTTAGA AATAAAATAT TATTCCCGCA CAAATGGAGA TGGATATTGA
101	TTTGGATGAT ATAGAAAATT TACTTCCTAA TACATTCAAC AAGTATAGCA
151	GCTCTTGTAG TGACAAGAAA GGATGCAAAA CATTGAAATC TGGCTCGAAA
201	TCGCCTTCAT TGACTATTCC AAAGTTGCAA AAACAATTAG AGTTCTACTT
251	CTCGGATGCA AATCTTTATA ACGATTCTTT CTTGAGAAAA TTAGTTTTAA
301	AAAGCGGAGA GCAAAGAGTA GAAATTGAAA CATTACTAAT GTTTAAATAA
351	AATCAGGTAA TGAGGATTAT TCTATTTTTT AGATCACTTC TTAAGGAGCA
401	TTATGGAGAA AATTACTTAA TACTAAAAGG TAAACAGTTT GGATTATTTC
451	CCTAGCCAAC AATGATGAGT ATATTAAATT CATATGAGAA TGAGTCAAAG
501	GATCTCGATA CATCAGACTT ACCAAAGACA AACTCGCTAT AAAACGCAAG
551	AAAAAGTTTG ATAATCGAAC AGCAGAAGAA CTTATTGCAT TTACTATTCG
601	TATGGGTTTT ATTACAATTG TTTTAGGTAT CGACGGTGAA CTCCCGAGTC
651	TTGAGACAAT TGAAAAAGCT GTTTACAACT GAAGGAATCG CAGTTCTGAA
701	AGTTCTGATG TGTATGCCAT TATTTTGTGA ATTAATCTCA AATATCTTAT
751	CTCAATTTAA TGGATAGCTA TAGAAACAAA CCAAATAAAC CATGCAAGTT
801	TAATGGAATA TACGTTAAAT CCTTTGGGAC AAATGCACAC TGAATTTATA
851	TTGGATTCTT AAAGCATAGA TACACAGAAT GCTTTAGAGA CTGATTTAGC
901	TTACAACAGA TTACCTGTTT TGATTACTCT TGCTCATCTC TTATATCTTT
951	
1001	
1051	
1101	
1151	
1201	
1251	
1301	
1351	
1401	
1451	
1501	
1551	
1601	
1651	
1701	AAGATTTATT TTTTTCAATA ATTTATTGAA AAGAGGGGTT TTGGGGTTTT

	1
a b c	PQNPKTPKPL * KKKKLR * FR - PKTPKPQNPYKKRKNCGSLE - PKPQNPKTPIKKEKIEVV * K-
	AATAAAATATTATTCCCGCACAAATGGAGATGGATATTGATTTGGATGATATAGAAAATT
	TTATTTATAATAAGGGCGTGTTTACCTCTACCTATAACTAAACCTACTATATCTTTTAA
a b c	N K I L F P H K W R W I L I W M I * K I - I K Y Y S R T N G D G Y C F G C Y R K F - * N I I P A Q M E M D I D L D D I E N L -
	TACTTCCTAATACATTCAACAAGTATAGCAGCTCTTGTAGTGACAAGAAAGGATGCAAAA
	121
a b c	Y F L I H S T S I A A L V V T R K D A K - T S * Y I Q Q V * Q L L * * Q E R M Q N - L P N T F N K Y S S S C S D K K G C K T -
	CATTGAAATCTGGCTCGAAATCGCCTTCATTGACTATTCCAAAGTTGCAAAAACAATTAG
	GTAACTTTAGACCGAGCTTTAGCGGAAGTAACTGATAAGGTTTCAACGTTTTTGTTAATC
a b c	H C N L A R N R L H C L F Q S C K N N · - I E I W L E I A F I D Y S K V A K T I R - L K S G S K S P S L T I P K L Q K Q L K -
	AGTTCTACTTCTCGGATGCAAATCTTTATAACGATTCTTTCT
	TCAAGATGAAGAGCCTACGTTTAGAAATATTGCTAAGAAAGA
a b c	S S T S R M Q I F I T I L S C E N * F * - V L L L G C K S L * R F F L E K I S F K - F Y F S D A N L Y N D S F L R K L V L K -
	AAAGCGGAGAGCAAAGAGTAGAAATTGAAACATTACTAATGTTTAAATAAA
	TTTCGCCTCTCGTTTCTCATCTTTAACTTTGTAATGATTACAAAATTTATTT
a	KAESKE• KLKHY• CLNKIR• -
c p	K R R A K S R N C N I T N V * I K S G N - S G E Q R V E I E T L L M F K * N Q V M -
	TGAGGATTATTCTATTTTTTAGATCACTTCTTAAGGAGCATTATGGAGAAAATTACTTAA
	361 420 ACTCCTAATAAGATAAAAATCTAGTGAAGAATTCCTCGTAATACCTCTTTTAATGAATT
a b c	C G L F Y F L D H F L R S I M E K I T · - E D Y S I F · I T S · G A L W R K L L N - R I I L F F R S L L K E H Y G E N Y L I -
	TACTAAAAGGTAAACAGTTTGGATTATTTCCCTAGCCAACAATGATGAGTATATTAAATT
	ATGATTTTCCATTTGTCAAACCTAATAAAGGGATCGGTTGTTACTACTCATATAATTTAA
a b c	Y · K V N S L D Y F P S Q Q C C V Y · I - T K R · T V W I I S L A N N D E Y I K F - L K G X Q F G L F P · P T M M S I L N S -

FIGURE 12 (cont.)

		CATATGAGAATGAGTCAAAGGATCTCGATACATCAGACTTACCAAAGACAAACTCGCTAT	540
	481	GTATACTCTACTCAGTTTCCTAGAGCTATGTAGTCTGAATGGTTTCTGTTTGAGCGATA	340
a b c	1	H M R M S Q R I S I H Q T Y Q R Q T R Y I C E C V K G S R Y I R L T K D K L A I Y E N E S K D L D T S D L P K T N S L *	-
	541	AAAACGCAAGAAAAAGTTTGATAATCGAACAGCAGAAGAACTTATTGCATTTACTATTCG TTTTGCGTTCTTTTTCAAACTATTAGCTTGTCGTCTTCTTGAATAACGTAAATGATAAGC	600
a b c	:	KTQEKVC * SNSRRTYCIYYS KRKKKFDNRTAEELIAFTIR NARKSLIIEQQKNLLHLLFV	-
	601	TATGGGTTTTATTACAATTGTTTTAGGTATCGACGGTGAACTCCCGAGTCTTGAGACAAT ATACCCAAAATAATGTTAACAAAATCCATAGCTGCCACTTGAGGGCTCAGAACTCTGTTA	660
a b c	,	Y G F Y Y N C F R Y R R C T P E S C D N M G F I T I V L G I D G E L P S L E T I W V L L Q L F · V S T V N S R V L R Q L	- - -
	661	TGAAAAAGCTGTTTACAACTGAAGGAATCGCAGTTCTGAAAGTTCTGATGTGTATGCCAT ACTTTTTCGACAAATGTTGACTTCCTTAGCGTCAAGACTTCCAAGACTACACATACGGTA	720
a b c	(CKSCLQLKESQFCKF * CVCH EKAVYNCRNRSSESSDVYAI KKLFTTEGIAVLKVLMCMPL	- - -
	721	TATTTTGTGAATTAATCTCAAATATCTTATCTCAATTTAATGGATAGCTATAGAAACAAA ATAAAACACTTAATTAGAGTTTATAGAATAGA	780
a b c	,	Y F V N · S Q I S Y L N L M D S Y R N K I L C I N L K Y L I S I · W I A I E T N F C E L I S N I L S Q F N G · L · K Q T	- - -
	781	CCAAATAAACCATGCAAGTTTAATGGAATATACGTTAAATCCTTTGGGACAAATGCACAC GGTTTATTTGGTACGTTCAAATTACCTTATATGCAATTTAGGAAACCCTGTTTACGTGTG	840
a b c	:	PNKPCKFNGIYVKSFGTNAH QINHASLMEYTLNPLGQMHT KTMQVWNIR ILWDKCTL	<u>-</u> -
	841	TGAATTTATATTGGATTCTTAAAGCATAGATACACAGAATGCTTTAGAGACTGATTTAGC ACTTAAATATAACCTAAGAATTTCGTATCTATGTGTCTTACGAAATCTCTGACTAAATCG	900
a b c	(CIYIGFLKHRYTECFRDCFS EFILDS SIDTQNALETDLA NLYWILKA IHRML RLI L	- -
	901	TTACAACAGATTACCTGTTTTGATTACTCTTGCTCATCTCTTATATCTTTAAAAGAAGCA AATGTTGTCTAATGGACAAAACTAATGAGAACGAGTAGAGAATATAGAAATTTTCTTCGT	960
a b c	i	LQQITCFDYSCSSLISLKEA YNRLPVEITLAHLLYL KKQ TTDYLFCLLLLISYIFKRSR	-
	961	GGCGAAATGAAAGAAGACTAAAGAAAGAGAGATTTCAAAATTTGTTGATTCTTCTGTAACC CCGCTTTACTTTTCTTCTGATTTCTTCTCTAAAGTTTTAAACAACTAAGAAGACATTGG	1020
a b c	•	G E M K R R L K K E I S K F V D S S V T A K C K E D · R K R F Q N L L I L L · P R N E K K T K E R D F K I C C F F C N R	
	1021	GGAATTAACAACAAGAATATTAGCAACGAAAAAGAAGAAGAGCTATCACAATCCTGATTC CCTTAATTGTTGTTCTTATAATCGTTGCTTTTTCTTCTTCTCGATAGTGTTAGGACTAAG	1080
a b c	•	G I N N K N I S N E K E E E L S Q S C F E L T T R I L A T K K K K S Y H N P D S N · Q Q E Y · Q R K R R R A I T I L I L	-

FIGURE 12 (cont.)

	1081	TTAAAGATTTCAAAAATTCCAGGTAAGAGAGATACATTCATT
		AATTTCTAAAGTTTTTAAGGTCCATTCTCTCTATGTAAGTAA
a b c		L K I S K I P G K R D T F I K I H I L * - * R F Q K F Q V R E I H S L K F I Y Y S - K D F K N S R * E R Y I H * N S Y I I V -
	1141	TTTTTCACTTCACAGCTGTTATTTCTTTTATCTTAACAATATTTTTTGATTAGCTGGAA 1200 AAAAAGTAAAGTGTCGACAATAAAAAGAAAATAGAATTGTTATAAAAAAACTAATCGACCTT
a b c		FFISQLLFSFILTIFFD ° LE - FSFHSCYFLLS ° QYFLISWK - FHFTAVIFFYLNNIFCLAGS-
	1201	GTAAAAAGTATCAAATAAGAGAAGCGCTAGACTGAGGTAACTTAGCTTATTCACATTCAT
a b c		V K S I K * E K R * T E V T * L I H I H - * K V S N K R S A R L R * L S L F T F I - K K Y Q I R E A L D C G N L A Y S H S *-
	1261	AGATCGACCTTCATATATCCAATACGATGATAAGGAAACAGCAGTCATCCGTTTTAAAAA
a b c		R S T F I Y P I R C * G N S S H P F * K - D R P S Y I Q Y D D K E T A V I R F K N - I D L H I S N T M I R K Q Q S S V L K I -
		TAGTGCTATGAGGACTAAATTTTTAGAGTCAAGAAATGGAGCCGAAATCTTAATCAAAAA
	1321	ATCACGATACTCCTGATTTAAAAATCTCAGTTCTTTACCTCGGCTTTAGAATTAGTTTTT
a b c		* C Y E D * I F R V K K W S R N L N Q K - S A M R T K F L E S R N G A E I L I K K - V L C G L N F * S Q E M E P K S * S K R -
	1381	GAATTGCGTCGATATTGCAAAAGAATCGAACTCTAAATCTTTCGTTAATAAGTATTACCA CTTAACGCAGCTATAACGTTTTCTTAGCTTGAGATTAGAAAGCAATTATTCATAATGGT
a b c		ELRRYCKRIEL IFR VLP - NCVDIAKESNSKSFVNKYYQ - IASILQKNRTLNLSLISITN -
	1441	ATCTTGATTGATGAAGAGATTGACGAGGCAACTGCACAGAAGATCATTAAAGAAATAAA 1500 TAGAACTAACTAACTTCTCTAAACTGCTCCGTTGACGTGTCTTCTAGTAATTTCTTTATTT
a b c		I L I D C R D · R G N C T E D H · R N K · S · L D C L K R L T R Q L H R R S L K K · S ·
	1501	GTAACTTTTATTAATTAGAGAATAAACTAAATTACTAATATAGAGATCAGCGATCTTCAA CATTGAAAATAATTAATCTCTTATTTGATTTAATGATTATATCTCTAGTCGCTAGAAGTT
a b c		V T F I N 'R I N 'I T N I E I S D L Q - L L L I R E ' T K L L I 'R S À I F N - N F Y ' L E N K L N Y ' Y R D Q R S S I -
	1561	TTGACGAAATAAAAGCTGAACTAAAAGTTAGACAATAAAAAAATACAAACCTTGGTCAAAAT AACTGCTTTÄTTTTCGACTTGATTTCAATCTGTTATTTTTATGTTTGGAACCAGTTTTA
a b c		L T K · X L N · S · T I K N T N L G Q N - C R N K S C T K V R Q · K I Q T L V K I - D E I X A E L K L D N K K Y K P W S K Y -
	1621	ATTGAGGAAGGAAAGAAGACCAGTTAGCAAAAGAAAAAATAAGCCAATAAATA
a		I E E G X E D Q L A K E K I R Q ' I K C -
a b c		LRKEXKTS OKKK GNK NE - CGRKRRPVSKRKNKAINKMS -

FIGURE 12 (cont.)

			'ACA	GA.	AGT	GAA	-	ATA													-	_	_				1740
	1681		тст	CT'	TCA	CŢŢ		TAT																			1740
a		v	Q	ĸ	С	R	N	к	R	F	I		F	F	N	1	N	L	Ĺ		ĸ	R	(G	v		-
ь		Y	R	S	ε	Ε	I	K	D] (F	F	S	;	r	Ι	Y		C	ĸ		Ε	G	F		-
С		Т	ε	'	,	K	K	•	K	I	Y	F		F	Q	•	1	F	I	Ε		K	R	C	; ;	۴ .	-
		TTC	CCC	TT	ттс	GGG	ттт	TGG	GG																		
	1741				- + -			+		176	52																
		AAC	ccc	:AA	AAC	CCC	AAA	ACC	CC																		
a		L	G	F	W	G	F	G		-																	
b		W	G	F	G	v	L	G		-																	
_		G	v	1	. (F	W		_																	

2 EVDVDNQADNHGIHSALKTCEEIKEAKTLYSWIQKVIRCRNQSQSHYKDL :::: : : : .:: . :: . .	51
19 ELELEMQENQNDIQVRVKIDDPKQYLVNVTAACLLQEGSYYQDK	62
52 EDIKIFAQTNIVATPRDYNEEDFKVIARKEVF.STGLMIELIDKCLVELL :: :: : : : . .	100
63 DERRYIITKALLEVAESDPEFICQLAVYIRNELYIRTTTNYIVAF.	107
101 SSSDVSDRQKLQCFGFQLKGNQLAKTHLLTALSTQKQYFFQDEWNQVRAM	150
108 CVVHKNTOPFIEKYFNKAVLLPNDLLEVCEFAQVLYI	144
151 IGNELFRHLYTKYLIFQRTSEGTLVQFCGNNVFDHLKVNDKFDKKQKGGA	200
:: :: .:::::. ::::::::::::::::	181
201 ADMNEPRCCSTCKYNVKNEKDHFLNNINVPNWNNMKSRTRIFYCTHF .:: .:: ::	247
182 SEFNEYQLGKYCTES. QRKKTMFRYLSVTNKQKWDQTKKK	220
248 NRNNQFFKKHEFVSNKNNISAMDRAQTIFTNIFRFNRIRKKLKDKVIEKI :::: :::: :::: :::: ::: - 221 .RKENLLTKLQAIKESEDKSKRETGDIMNVEDAIKALKPAVMKKI	297
	264
298 AYMLEKVKDFNFNYYLTKSCPLPENWRERKQKIENLINKTREEKSKYYEE 	347
. : : .	294
348 LFSYTTDNKCVTQFINEFFYNILPKDFLTGRNRKNFQKKVKKYVELNKHE	397
295 LIKFCHISEPKERVYKILGKKYPKTEEEYKAAFGDSASAPFN.PE	338
398 LIHKNLLLEKINTREISWMQVETSAKHFYYFDHENIYVLWKLLRWIFEDL	447
339 LAGKRMKIEISKTWENELSAKGNTAEVWDNLISSNQLPYMAMLRNLSN.	386
448 VVSLIRCFFYVTEQQKSYSKTYYYRKNIWDVIMKMSIADLKKETLAEVQE	497
387ILKAGVSD	394
498 KEVEEWKKSLGFAPGKLRLIPKKTTFRPIMTFNKKIVNSDRKTTKLTTNT	547
395	398 597
548 KLLNSHLMLKTLKNRMFKDPFGFAVFNYDDVMKKYEEFVCKWKQVGQPKL ::	415
399 IVINK ICEPKAVENSKM	647
598 FFATMDIEKCYDSVNREKLSTFLKTTKULSSDFWIMTAQILKRKNNIVID '::::: :::: ::: :: :: 416 F. PLQFFSAIEAVN EAVTKGFKAKK RENMNLKGQIEAVKE VVE	457
	597
548 SKNFRKKEMKDYFRQKFQKIALECGQYPTLFSVLENEQNDLNAKKTLIVE .	496
698 AKQRNYFKKDNLLQPVINICQYNYINFNGKFYKQTKGIPQGLCVSSILSS	
### ##################################	546
748 FYYATLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLITTQENNAVLFI	797
: . : : : . : : : : :	57€
798 EKILINVSRENGFKFNMKK.LOTSFPLSPSKFAKYGMDSVEEQNIVQDYCD	846
.::::: ::: .:: :::	
847 WIGISIDMKTLALMPNINLRIEGILCTLNLNMQTKKASMWLKKKLKSFLM	896
	653
897 NNITHYFRKTITTEDFANKTLNKLFISGGYKYMQCAKEYKD.HFKKNLAM	945
	687
946 SSMIDLEVSKILYSVTRAFFKYLVCNIKDTIFGEEHYPDFFLSTLKHFIE	995
	706
996 IFSTKKYIFNRVC 1008	- -
// Al GIRALLIMITE	

	: : : : :	43
179	GNNVFDHLKVNDKFDKKQKGGAADMNEPRCCSTCKYNVKNEKDHFLNNIN	228
44	:::: ::: : KEEDLKLLKFKNQDQDGNSGNDDDDEENNSNKQQELLRRVN	84
229	VPNWNNMKSRTRIFYCTHFNRNNQFFKKHEFVSNKNNISAMDRAQTIFTN :: :: :. :	278
85	QIKQQVQLIKKVGSKVEKDLNLNEDENKKN	114
279	<pre>IFRFNRIRKKLKDKVIEKIAYMLEKVKDFNFNYYLTKSCPLPENWRERKQ :: :: : :::: :: .</pre>	328
115	GLSEQOVKEEQLRTITEEQVKYQNLVFNMDYQLDLNESGGHRRHRRETDY	164
329	KIENLINKTREEKSKYYEELFSYTTONKCVTQFINE.FFYNILPKDFLTG	377
165	.::: ::: :: :: :: ::: DTEKWFEISHDQKNYVSIYANQKTSYCWWLKDYFNK	200
378	RNRKNFQKKVKKYVELNKHELIHKNLLLEKINTREISWMQVETSAKHFYY	427
201	NNYDHLNVSINRLE. TEAEFYAFDDFSQTIKLTNNSYQTVNID	242
428	FDHENIYVLWKLLRWIFEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNI .: : : : : : :	475
243	VNFDNNLCILALLRFLLSLERFNILNIRSSY TRNQYNFEKIGELLETI	290
476	WDVIMKMSIADLKKETLAEVQEKEVEEWKKSLGFAPGKLRLIPKKTTFRP	525
291	: ::. : : ::: FAVVFSHR HLQGIHLQVPCEAFQYLVNSSSQISVKDSQLQ	330
526	IMTFNKKIVNSDRKTTKLTTNTKLLNSHLMLKTLKNRMFKDPFGFAVFNY :	575
331	VYSFSTDLKLVD. TNKVQDYFKFLQEFPRLTHVSQQAIPVSATNAVENL	378
576 379	DDVMKKYEEFVCKWKQVGQPKLFFATMDIEKCYDSVNREK ::: : . : ::: : NVLLKKVKHANLNLVSIPTQFNFDFYFVNLQHLKLEFGLEPNILTKQK	615 426
516	LSTFLKTTKLLSSDFWIMTAQILKRKNNI.VIDSKNFRKKEMK	657
427	. .	476
558	DYFROKFOKIALEGGOYPTLFSVLENEQNDLNAKKTLIVEAKORNYFK	705
477	EETPETKDETPSESTSGMKFFDHLSELTELEDFSVNLQATQEIY	520
706	KDNELOPVINICQYNYINFNGKFYKQTKGIPQGLCVSSILSSFYYATLEE	755
521	.DSLHKLLIRSTNLKKFKLSYKYEMEKSKMDTFIDLKNIYETLNN	564
756	SSLGFLRDESMNPENPNVNLLMRLTDDYLLITTQENNAVLFIEKLINVSR	805
565	: : . : : :: LKRCSVNISNPHGNISYELTNKDSTFYKFKLTLNQE	600
806	ENGFKFNMKKLQTSFPLSPSKFAKYGMDSVEEQNIVQDYCDWIGISIDMK	855
601	LQHAKYTFK QNEFQFNNVKSAKIESSSLESLEDIDSLCKSIASCKNLQ	648
856	TLALMPNINLRIEGILCTUNLNMQT. KKASMWLKK. KLKSFLMNNITH	901
649	NVNI IASLLYPHNIQKNPFNKPNLLFFKQFEQLKNLENVSINC	691
902	YFRKTI. TTEDFANKTLNKLFISGGYKYMQCAKEYKDHFKKNLAMSSM	948
692	ILDQHILNSISEFLEKNKKIKAFILKRYYLLQYYLDYTKLFKTLQQLPEL	741
949	IDLEVSKIIYSVTRAFFKYLVCNIKDTIFGEEHY :: : : : : : : ::	982
742	NQVYINQQLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSQTLQLIDF	791
983		1028
792	DQNTVSDDSIKKILESISESKYHHYLRLNPSQSSSLIKSENEEIQELLK	840

	DIDLDDIENLLPNTFNKYSSSCSDKKGCKTLKSGSKSPSLTIPK	47
<i>(</i>) 3	:: H : : : :	
617	NVKSAKIESSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPNNIQKNP	666
48	LQKQLEFYFSDANLYNDSFLRKLVLKSGEQRVE IETLLM	
667	: : : ::: . : . . : : ::: FNKPNLLFFKQFEQLKNLENVSINCILDOHILNSISEFLEKNKKIKAFIL	

	MEMDIOLDDIENLLPNTFNKYSSSCSDKKGCKTLKSGSKSPS	
491	IELAIKIAVNKNLDEIKGHTAIFSDVSGSMSTSMSGGAKKYGSVRTCLEC	540
43	LTIPKLOKOLEFYFSDANLYNDSFLRKLVLKSGEORVEIETLL	85
541	ALVICIMOKORCEKSSEYTESSPSSOCNKCYL EVDLPGDELRPSMOKLL	589

FIGURE 17

Motif A

Motif B

SILSSFYYATLEESSLGFL PUMECLALNPLSHQLHNDR PALCNAVILRIDRRLAGLA SPAIFOSSMTKILEPFRKON 3A ? I VD LVYDDL LE FYSEPK LKKKKSVTVLDVGDAYFSVPLDEDFRKYTAFTIP- 7-SIRYQYNVLP VLPELYFMKFDVKSCYDSIPRMECMRILKDALKN- 68-KCYIREDGLF 26-HVPVGPRVCV GQPKLFPATMDI EKCYDSVNREKLSTFLKTTKUL-100-KFYRQTKGI F 28-RQIAIKKGIY h - - - C KARNEHCTY IDYKKAEDS I PHSWEIQVEEIYKIN-FGGSNWFREVELKKCFDT I SHDEI I KELKRY I SD-4--h----h---h al S.c.(groupII)FGGSNWFREV telomerase p123 L8543.12 years Dong (LINE) Consensus HIV-RT

Motif C

Motif D

Motif B

h-high-h PANT 4 - ETPARFI SLOT - 23 - QDYCDWI CKT-25-KCJYKYL O-EPPFLWM 8-ILKLADDFLIISTDQQQ......VINIKKLAMGGPQKYNAKANR-41 gh-h--4 SPX PANA 5-YVRYADDILIGVLGSKA-2-KIIKRDLNNFLNS.LGLTINEE 4-IYQYMDDLYVGSHLEIG-1-HRTKIRELRQHLLRWGLTFDR -16-HLIYMDDIKLYAKNDKE-0-MKKLIDTTTIFSNDISMQYGLD OYLLITYQENN-0-AVLFIEKLINVSREN h--release al S.c.(groupII)-55-YVRYAD -14-LMBLT telomerase p123 L8543.12 YAM Dong (LINE) Consensus HIV-RT

telomerase p43 human La Xenopus LaA Drosophila La S. c. Lhplp LQKQ1EFYSSDANLYNDSFLRKLVLKSGEQRVEIETLLM ICHQLEYYFGDFNLPRDKFLKEQI.KLDEGWVPLEIMIK ICEQIEYYFGDHNLPRDKFLKQQI.LLDDGWVPLETMIK ILRQVEYYFGDANLNRDKFLREQIGKNEDGWVPLSVLVT CLKOMEFYESEFNFPYDRFLRTTAEK.NDGWVPISTIAT

1	aacteatta attactaatt taateaacaa gattgataaa aageagtaaa taataeeea
61	tagatttaat ttagaaagta tcaattgaaa aatggaaatt gaaaacaact aagcacaata
121	gccaaaagcc gaaaaattgt ggtgggaact tgaattagag atgcaagaaa accaaaatga
181	tatataagtt agggttaaga ttgacgatcc taagcaatat ctcgtgaacg tcactgcagc
241	atgtttgttg taggaaggta gttactacta agataaagat gaaagaagat atatcatcac
301	taaagcactt cttgaggtgg ctgagtctga tcctgagttc atctgctagt tggcagtcta
361	catccgtaat gaactttaca tcagaactac cactaactac attgtagcat tttgtgttgt
421	ccacaagaat actcaaccat tcatcgaaaa gtacttcaac aaagcagtac ttttgcctaa
	tgacttactg gaagtctgtg aatttgcata ggttctctat atttttgatg caactgaatt
541	caaaaatttg tatettgata ggataettte ataagatatt egtaaggaae teaettteeg
60 l	taagtgttta caaagatgcg tcagaagcaa gttttctgaa ttcaacgaat actaacttgg
66 l	taagtattgc actgaatcct aacgtaagaa aacaatgttc cgttacctct cagttaccaa
721	caagtaaaag tgggattaaa ctaagaagaa gagaaaagag aatctcttaa ccaaacttta
781	ggcaataaag gaatctgaag ataagtccaa gagagaaact ggagacataa tgaacgttga
841	agatgcaatc aaggctttaa aaccagcagt tatgaagaaa atagccaaga gatagaatgc
901	catgaagaaa cacatgaagg cacctaaaat tectaactet acettggaat caaagtaett
961	gacetteaag gateteatta agttetgeea tatttetgag eetaaagaaa gagtetataa
102	l gateettggt aaaaaataee etaagaeega agaggaatae aaageageet ttggtgatte
108	l tgcatctgca cccttcaatc ctgaattggc tggaaagcgt atgaagattg aaatctctaa
114	l aacatgggaa aatgaactca gtgcaaaagg caacactgct gaggtttggg ataatttaat
120	l ttcaagcaat taactcccat atatggccat gttacgtaac ttgtctaaca tcttaaaagc
126	l eggtgtttea gatactaeae actetattgt gateaaeaag atttgtgage ecaaggeegt
132	l tgagaactcc aagatgttcc ctcttcaatt ctttagtgcc attgaagctg ttaatgaagc
138	l agttactaag ggattcaagg ccaagaagag agaaaatatg aatcttaaag gtcaaatcga
144	l agcagtaaag gaagttgttg aaaaaaccga tgaagagaag aaagatatgg agttggagt
150	l aaccgaagaa ggagaatttg ttaaagtcaa cgaaggaatt ggcaagcaat acattaactc
156	l cattgaactt gcaatcaaga tagcagttaa caagaattta gatgaaatca-aaggacacac
162	l tgcaatette tetgatgttt etggttetat gagtacetea atgteaggtg gageeaagaa
	l gtatggttcc gttcgtactt gtctcgagtg tgcattagtc cttggtttga tggtaaaata
	l acgttgtgaa aagtcctcat tctacatctt cagttcacct agttctcaat gcaataagtg
	l ttacttagaa gttgatetee etggagaega aeteegteet tetatgtaaa aaettttgea
	l agagaaagga aaacttggtg gtggtactga tttcccctat gagtgcattg atgaatggac
	l aaagaataaa actcacgtag acaatatcgt tattttgtct gatatgatga ttgcagaagg
	l atattcagat atcaatgtta gaggcagttc cattgttaac agcatcaaaa agtacaagga
	l tgaagtaaat cctaacatta aaatctttgc agttgactta gaaggttacg gaaagtgcct
	l taatctaggt gatgagttca atgaaaacaa ctacatcaag atattcggta tgagcgattc
	l aatettaaag tteattteag eeaageaagg aggageaaat atggtegaag ttateaaaaa
	l ctttgccctt caaaaaatag gacaaaagtg agtttcttga gattcttcta taacaaaaat
	l ctcaccccac ttttttgttt tattgcatag ccattatgaa atttaaatta ttatctattt
234	l atttaagtta cttacatagt ttatgtatcg cagtctatta gcctattcaa atgattctgc
240	1 nonggorgan nangattana n

MEIENNQAQQPKAEKLWWELELEMQENQNDIQVRVKIDDPKQYL
VNVTAACLLQEGSYYQDKDERRYIITKALLEVAESDPEFICQLAVYIRNELYIRTTTN
YIVAFCVVHKNTQPFIEKYFNKAVLLPNDLLEVCEFAQVLYIFDATEFKNLYLDRILS
QDIRKELTFRKCLQRCVRSKFSEFNEYQLGKYCTESQRKKTMFRYLSVTNKQKWDQTK
KKRKENLLTKLQAIKESEDKSKRETGDIMNVEDAIKALKPAVMKKIAKRQNAMKKHMK
APKIPNSTLESKYLTFKDLIKFCHISEPKERVYKILGKKYPKTEEEYKAAFGDSASAP
FNPELAGKRMKIEISKTWENELSAKGNTAEVWDNLISSNQLPYMAMLRNLSNILKAGV
SDTTHSIVINKICEPKAVENSKMFPLQFFSAIEAVNEAVTKGFKAKKRENMNLKGQIE
AVKEVVEKTDEEKKDMELEQTEEGEFVKVNEGIGKQYINSIELAIKIAVNKNLDEIKG
HTAIFSDVSGSMSTSMSGGAKKYGSVRTCLECALVLGLMVKQRCEKSSFYIFSSPSSQ
CNKCYLEVDLPGDELRPSMQKLLQEKGKLGGGTDFPYECIDEWTKNKTHVDNIVILSD
MMIAEGYSDINVRGSSIVNSIKKYKDEVNPNIKIFAVDLEGYGKCLNLGDEFNENNYI
KIFGMSDSILKFISAKQGGANMVEVIKNFALQKIGQK

l tcaatactat taattaataa ataaaaaaaa gcaaactaca aagaaaatgt caaggcgtaa 61 ctaaaaaaag ccataggctc ctataggcaa tgaaacaaat cttgattttg tattacaaaa 121 tctagaagtt tacaaaagcc agattgagca ttataagacc tagtagtaat agatcaaaga 181 ggaggatete aagettttaa agtteaaaaa ttaagattag gatggaaact etggeaacga 241 tgatgatgat gaagaaaaca actcaaataa ataataagaa ttattaagga gagtcaatta 301 gattaagtag caagtttaat tgataaaaaa agttggttct aaggtagaga aagatttgaa 361 tttgaacgaa gatgaaaaca aaaagaatgg actttctgaa tagcaagtga aagaagagta 421 attaagaacg attactgaag aataggttaa gtattaaaat ttagtattta acatggacta 481 ccagttagat ttaaatgaga gtggtggcca tagaagacac agaagagaaa cagattatga 541 tactgaaaaa tggtttgaaa tatctcatga ccaaaaaaat tatgtatcaa tttacgccaa 601 ctaaaagaca tcatattgtt ggtggcttaa agattatttt aataaaaaca attatgatca 661 tettaatgta ageattaaca gaetagaaac tgaageegaa ttetatgeet ttgatgattt 721 ttcacaaaca atcaaactta ctaataattc ttactagact gttaacatag acgttaattt 781 tgataataat ctctgtatac tcgcattgct tagattttta ttatcactag aaagattcaa 841 tattttgaat ataagatett ettatacaag aaattaatat aattttgaga aaattggtga 901 getacttgaa actatetteg eagttgtett tteteatege eaettacaag geatteattt 961 acaagtteet tgegaagegt tetaatattt agttaaetee teateataaa ttagegttaa 1021 agatagetaa ttataggtat aetetttete tacagaetta aaattagttg acactaacaa 1081 agtccaagat tattttaagt tettataaga atteeetegt ttgactcatg taagetagta 1141 ggctatccca gttagtgcta ctaacgctgt agagaacctc aatgttttac ttaaaaaggt 1201 caagcatgct aatcttaatt tagtttctat ccctacctaa ttcaattttg atttctactt 1261 tgttaattta taacatttga aattagagtt tggattagaa ccaaatattt tgacaaaaca 1321 aaagettgaa aatetaettt tgagtataaa ataateaaaa aatettaaat ttttaagatt 1381 aaacttttac acctacgttg cttaagaaac ctccagaaaa cagatattaa aacaagctac 1441 aacaatcaaa aatctcaaaa acaataaaaa tcaagaagaa actcctgaaa ctaaagatga 1501 aactccaagc gaaagcacaa gtggtatgaa attttttgat catctttctg aattaaccga 1561 gettgaagat tteagegtta aettgtaage taeccaagaa atttatgata gettgeacaa 1621 acttttgatt agatcaacaa atttaaagaa gttcaaatta agttacaaat atgaaatgga 1681 aaagagtaaa atggatacat tcatagatct taagaatatt tatgaaacct taaacaatct 1741 taaaagatgc tetgttaata tatcaaatec teatggaaac atttettatg aactgacaaa 1801 taaagattet aetttttata aatttaaget gaeettaaae taagaattat aacaegetaa 1861 gtatactttt aagtagaacg aattttaatt taataacgtt aaaagtgcaa-aaattgaatc 1921 ttccicatta gaaagettag aagatattga tagtetttge aaatetattg ettettgtaa 1981 aaatttacaa aatgttaata ttatcgccag tttgctctat cccaacaata tttagaaaaa 2041 teettteaat aageeeaate ttetatttti caageaattt gaataattga aaaatttgga 2101 aaatgtatet ateaaetgta ttettgatea geatataett aattetattt eagaattett 2161 agaaaagaat aaaaaaataa aagcattcat tttgaaaaga tattatttat tacaatatta 2221 tettgattat aetaaattat ttaaaacaet teaatagtta eetgaattaa attaagttta 2281 cattaattag caattagaag aattgactgt gagtgaagta cataagtaag tatgggaaaa 2341 ccacaagcaa aaagctttct atgaaccatt atgtgagttt atcaaagaat catcctaaac 2401 cetttageta atagattttg accaaaacae tgtaagtgat gaetetatta aaaagatttt 2461 agaatetata tetgagteta agtateatea ttatttgaga ttgaaceeta gttaatetag 2521 cagtttaatt aaatetgaaa acgaagaaat ttaagaactt ctcaaagett gegacgaaaa 2581 aggtgtttta gtaaaagcat actataaatt ccctctatgt ttaccaactg gtacttatta 2701 tgaatatttc tttgcttatt atttgaataa tacatacaat agtcattttt agtgttttga 2761 atatatttta gttatttaat tcattatttt aagtaaataa ttatttttca atcatttttt 2821 aaaaaaatcg

MSRRNQKKPQAPIGNETNLDFVLQNLEVYKSQIEHYKTQQQQIK EEDLKLLKFKNQDQDGNSGNDDDDEENNSNKQQELLRRVNQIKQQVQLIKKVGSKVEK DLNLNEDENKKNGLSEQQVKEEQLRTITEEQVKYQNLVFNMDYQLDLNESGGHRRHRR ETDYDTEK WFEISHDQKNYVSIYANQKTSYCWWLKDYFNKNNYDHLNVSINRLETEAE FYAFDDFSQTIKLTNNSYQTVNIDVNFDNNLCILALLRFLLSLERFNILNIRSSYTRN QYNFEKIGELLETIFAVVFSHRHLQGIHLQVPCEAFQYLVNSSSQISVKDSQLQVYSF STDLKLVDTNKVQDYFKFLQEFPRLTHVSQQAIPVSATNAVENLNVLLKKVKHANLNL VSIPTQFNFDFYFVNLQHLKLEFGLEPNILTKQKLENLLLSIKQSKNLKFLRLNFYTY VAQETSRKQILKQATTIKNLKNNKNQEETPETKDETPSESTSGMKFFDHLSELTELED FSVNLQATQEIYDSLHKLLIRSTNLKKFKLSYKYEMEKSKMDTFIDLKNIYETLNNLK RCSVNISNPHGNISYELTNKDSTFYKFKLTLNQELQHAKYTFKQNEFQFNNVKSAKIE SSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPNNIQKNPFNKPNLLFFKQFEQLK NLENVSINCILDQHILNSISEFLEKNKKIKAFILKRYYLLQYYLDYTKLFKTLQQLPE LNQVYINQQLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSQTLQLIDFDQNTVSD DSIKKILESISESKYHHYLRLNPSQSSSLIKSENEEIQELLKACDEKGVLVKAYYKFP **LCLPTGTYYDYNSDRW**

MKILFEFIQDKLDIDLQTNSTYKENLKCGHFNGLDEILTTCFAL PNSRKIALPCLPGDLSHKAVIDHCIIYLLTGELYNNVLTFGYKIARNEDVNNSLFCHS ANVNVTLLKGAAWKMFHSLVGTYAFVDLLINYTVIQFNGQFFTQIVGNRCNEPHLPPK WVORSSSSATAAQIKQLTEPVTNKQFLHKLNINSSSFFPYSKILPSSSSIKKLTDLR EAIFPTNLVKIPQRLKVRINLTLQKLLKRHKRLNYVSILNSICPPLEGTVLDLSHLSR OSPKERVLKFIIVILQKLLPQEMFGSKKNKGKIIKNLNLLLSLPLNGYLPFDSLLKKL RLKDFRWLFISDIWFTKHNFENLNQLAICFISWLFRQLIPKIIQTFFYCTEISSTVTI VYFRHDTWNKLITPFIVEYFKTYLVENNVCRNHNSYTLSNFNHSKMRIIPKKSNNEFR IIAIPCRGADEEEFTIYKENHKNAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKE FKORLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMRILKDALKNENGFFVRSQYFFN TNTGVLKLFNVVNASRVPKPYELYIDNVRTVHLSNQDVINVVEMEIFKTALWVEDKCY IREDGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPSQDTLILKLADDFLIISTDQQQV INIKKLAMGGFQKYNAKANRDKILAVSSQSDDDTVIQFCAMHIFVKELEVWKHSSTMN NFHIRSKSSKGIFRSLIALFNTRISYKTIDTNLNSTNTVLMQIDHVVKNISECYKSAF KDLSINVTQNMQFHSFLQRIIEMTVSGCPITKCDPLIEYEVRFTILNGFLESLSSNTS KFKDNIILLRKEIQHLQAYIYIYIHIVN

Oxytricha Euplotes LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT LCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLT

	i e e e e e e e e e e e e e e e e e e e
human tez1 EST2 p123	Motif 0 AKFLHWLMSVYVVELLRSFFYVTETTFQKNR ISEIEWLVLGKRSNAKMCLSDFEKRKQIFAEFIYWLYNSFIIPILQSFFYITESSDLRNR LKDFRWLFISDIWFTKHNFENLNQLAICFIBWLPRQLIPKIIQTFFYCTEISSTVT- TREISWMQVET-SAKHPYYFDHEN-IYVLWKLLRWIFEDLVVSLIRCFFYVTEQQKSYSK
human tezl EST2 Dp123	Motif 1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVSEAEVRQHREARPALLTSRLRFIPKPDGL TVYFRKDIWKLLCRPPI-TSMKMEAFEKINENNVRMDTQK-TTLPPAVIRLLPKKNTF IVYFRHDTWNKLITPFIVEYFKTYLVENNVCRNHNSYTLSMFNHSKMRIIPKKSNNEF TYYYRKNIWDVIMKMSI-ADLKKETLAEVQEKEVEEWKKS-LGFAPGKLRLIPKKTTF
Fhuman tez1 E812 p123	Hotif 2 RPIVNHDYVVGARTFRREKRAERLTSRVKALF-SVLNYERA RLITN-LRKRFLIKMGSNKKMLVSTNQTLRPVASILKHLINEESSGIPFNLEVYHKLLTF RIIAIPCRGADEEEFTIYKENHKNAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKEF RPIMTFNKKIVNSDRKTTKLTTNTKLLNSHLMLKTLKN-RMFKDPPGPAVFNYDDVMKKY * * * * * * * * * * * * * * * * * * *
tezl EST2 p123	Motif 3 (A) KKDLLKHRMFGR-KKYFVRIDIKSCYDRIKQDLMFRIVKK-KLKDPEPVIRKYATIHATS KQRLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMRILKD-ALKNENGFFVRSQYFFNTN EBFVCKWKQVGQPKLPFATMDIEKCYDSVNREKLSTFLKTTKLLSSDFWIHTAQILKRKW

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GTGCTCAACTACGAGCGGCGCG

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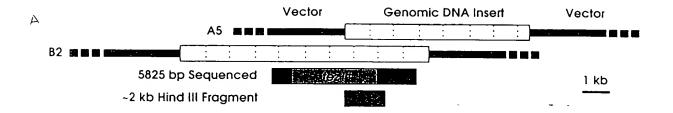
FIGURE 30 (cont.)

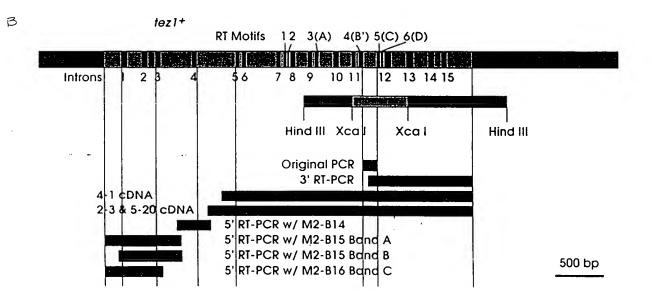
EST2 pep Euplotes pep Trans of tetrahymen	FFYCTEISST VTIVYFRHDT WNKLIT PFIVE YFK-TYLVEN FFYVTEQQKS YSKTYYYRKN IWDVI-MKMS DADLKK ETLAEVQEKHKE GSQIFYYRKP IWKLVSKLTI VKVRIQFSEK NKQMKNNFYQ	43 44
Consensus	FFY.TEKSYYYRK. IWKLFKV	50
EST2 pep Euplotes pep Trans of tetrahymen Consensus	NVCRNHNSY TLSNFNHSKM FULLEKKSNNE FRUIAIPCRG KEVEEWKKSLGFAPCKG FULLEKKIT FREIMTFNKK KIQLEEENLE KVEEKLIPED SFQKYPOXK FULLEKKS FREIMTFLRK K. E	78 92
EST2 pep . Euplotes pep Trans of tetrahymen Consensus	ADEEDFTIYK ENHKNAIQPT OKILEYERIK RPTSFTKIYS PTQIADRIKE IVNSDRKTTK LTTNTKLING HLMLKTIKNRMFK -DPFGFAVFN DKQKNIK LNINQILMDS OLVFRNIKDML-G -QKIGYSVFDK.KLN.N.L.SQL.L.LKN	120
EST2 pep Euplotes pep Trans of tetrahymen Consensus	FKORLLKKEN NVL PETLYFMKFD VKSCYD YD-DVMKKYE EFVCKWKQVG CFKUFFATMD IEKCYD NK-QISEKFA QFIEKWXNKG RECTYVTLKKKFFKWKG. ELLYF.T.DCYD	157 155 158 186

S-1: FFY VTE TTF QKN RLF FYR KSV WSK

S-2: ROH LKR VOL RDV SEA EVR OHR EA S-3: ART FRR EKR AER LTS RVK ALF SVL NYE

A-1: AKF LHW LMS VYV VEL LRS FFY VTE TTF Q A-2: LFF YRK SVW SKL QSI GIR QHL KRV QLR DVS A-3: PAL LTS RLR FIP KPD GLR PIV NMD YVV





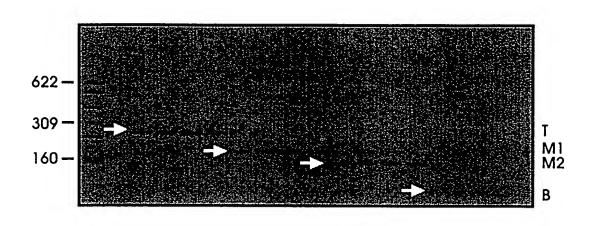
Poly 4

t t c
ta a g c c t c g
5'- cag acc aaa gga att cca taa gg -3'
Q T K G I P Q G

4 (B')

5 (c')

DDYLLIT 3'- ctg ctg atg gag gag tag tgg -5' a a a a a a a a a t t t t c c Poly 1



Motif B' (4)

QTKGIPQG

Motif C (5)

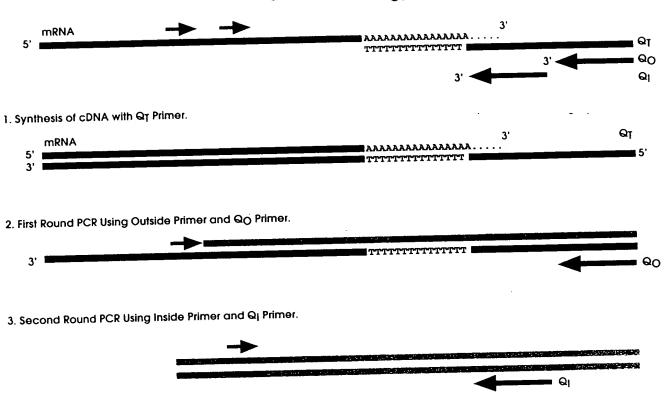
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PCR Product M2 showed Reasonable Match with Other Telomerase Proteins

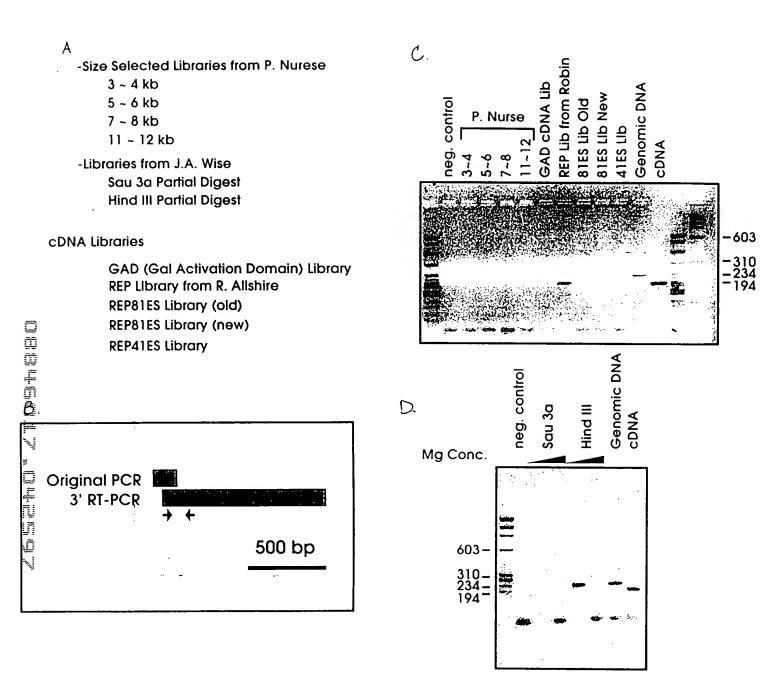
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  Ea_p123
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                      SILSSFLCHFYMEDLIDEYLSFTKKK-----GSVLLRVV
  Sp M2
  Sc_p103
               DGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPS-----QDTLILKLADDFLIIS
    K V G I P Q G
  caa aaa gtt ggt atc cct cag gg..... <---Actual Genomic Sequence.
  Poly 4
Œ
              t
           g c c t c g
  cag acc aaa gga att cca taa gg ---->
   ag acc aaa gga att cca tca ggC TCA ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG
   tc tgg ttt cct taa ggt agt ccG AGT TAA GAC AGT AGA AAA AAC ACA GTA AAG ATA TAC
" LI L
                       S
                           G
                               S
                                  I
                                     L
                                         S
                                             S
                                                    L
                                                        C
GAA GAT TTG ATT GAT GAA TAC CTA TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA
🛂 CTT CTA AAC TAA CTA CTT ATG GAT AGC AAA TGC TTT TTC TTT CCT AGT CAC AAC AAT GCT
                    Ε
                       Y
                           L
                               S
                                  F
                                      Т
                                         K
                                             K
                                                K G
                                                        S
  GTA GTC gac gac tac ctc ctc atc acc
  CAT CAG ctg ctg atg gag gag tag tgg
    V D
            D Y
                    L L
                           Ι
    <---- ctg ctg atg gag gag tag tgg
           a a aaaaa
                     t
                         t
                             t t
                         C
                     С
                             Poly 1
     .....gac gat ttc ctc ttt ata aca...... <---Actual Genomic Sequence.
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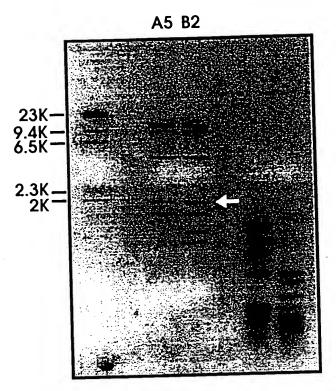
DDFLFI

3' RT PCR Strategy

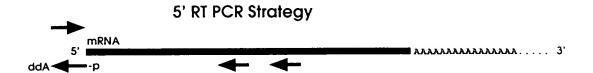


4. Sequence Second Round PCR Products Using Inside Primer or Q₁ Primer.

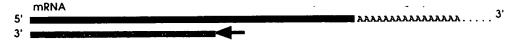




Hind III Digested Positive Genomic Clones



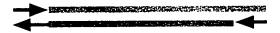
1. Synthesis of cDNA with Specific Downstream Primer.



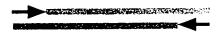
2. Ligate Oligo with 5'-P and blocked 3' to cDNA using T4 RNA Ligase.



3. First Round PCR



4. Second Round PCR



Alignment of RT Domains from Telomerase Catalytic Subunits.

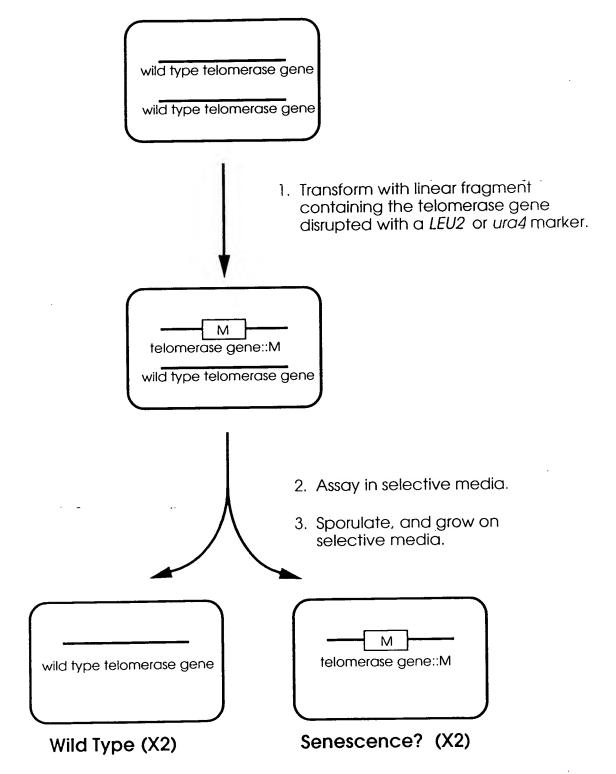
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Motif O
S.p. Tez1p (429). WLYNSFIIPILQSFFYITESSDLRNRTVYFRKDIW ...(35)...
S.c. Est2p (366). WLFRQLIPKIIQTFFYCTEISSTVT-IVYFRHDTW ...(35)...
           (441). WIFEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNIW ...(35)...
E.a. p123
            Motif 1
                        Motif 2
                                    K
            p hh h K
                         hR h
            AVIRLLPKK--NTFRLITN-LRKRF ...(61)...
S.p. Tezlp
            SKMRIIPKKSNNEFRIIAIPCRGAD ...(62)...
S.c. Est2p
E.a. p123
            GKLRLIPKK--TTFRPIMTFNKKIV ... (61)...
                * * *
            Motif 3(A) AF
               h hDh GY
                           h
            KKYFVRIDIKSCYDRIKQDLMFRIVK ...(89)...
S.p. Tezlp
            ELYFMKFDVKSCYDSIPRMECMRILK ... (75)...
S.c. Est2p
E.a. p123
            KLFFATMDIEKCYDSVNREKLSTFLK ...(107)...
             Motif 4(B')
                  hPOG
                         pP hh
                                 h
            YLQKVGIPQGSILSSFLCHFYMEDLIDEYLSF ...(6)...
S.p. Tezlp
S.c. Est2p
            YIREDGLFQGSSLSAPIVDLVYDDLLEFYSEF
            YKOTKGIPOGLCVSSILSSFYYATLEESSLGF
E.a. p123
                Y Motif 5(C)
                                              Motif 6(D)
                                              Gh h cK h
               F DDhhh
S.p. Tezlp
            VLLRVVDDFLFITVNKKDAKKFLNLSLRGFEKHNFSTSLEKTVINFENS . (205)
            LILKLADDFLIISTDQQQVINIKKLAMGGFQKYNAKANRDKILAVSSQS .(173)
S.c. Est2p
E.a. p123 ~
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```

A

FIGURE 42

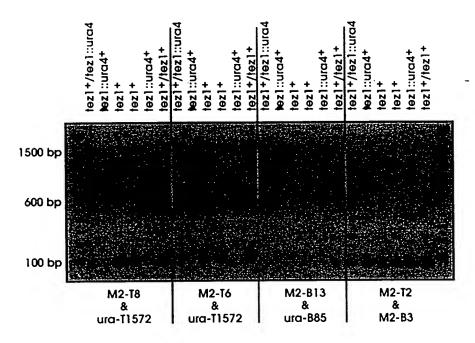
Sp_TD10 "YVKOMEDE FERRE WINTERSHIP 12 SC_ESSO "ILVE TOELVM ... Y TYKIAR ED ... " SP_TRIP IN SOUNTY SEGSET FALPHONY LT SELPLEN IN SELECTION TO SELECT SELECTION TO SE Sp_TIDID 30 MEKISEE VLGKRSNAKHCLSE KRKEIFA 405 SC_EMEZD 30 ILRLKDFR FIS---DIWETKHEE LNELLI 30 MATRIES MOVETS - AKHTEKH VYEWS - IVVU 40 SO_TIPIP ON ESTYPHYNSFIPPLES I STATE I Sp. TIDID ... FROM HE REST TO MAKE RECT OF THE REST OF So_Tip1p 640 FKYMPCFEQLIYOMOSLTDLIKPLRPYTRQVLF 641
Sc_EAZD 640 TS......KPKONIILLRKEIOHDQAYIY 877
Ea_p123 644 IEIFS...TKKYIMINRVCMILKAKEAKMEKSDQC 6023 Sp.Tptp +== FKYHPCFEQLIM CO QSLTD IMPLRPYROYLF HI Sc.Ext2p +== TS - - - - - - - - K KONII MERKEIOH QAYIY s7 En.D123 +== IEIFS - - TKKMII NAYCHIM AKEAK KSOOC 1022 Sp_Tip1p sez LHRREAD -Sc_Est2p sts IVIKEVH -Es_p123 ses OSLIOYEA

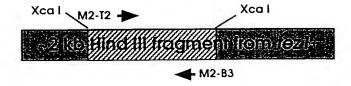
FIGURE 43
Disruption strategy for the putative telomerase genes.

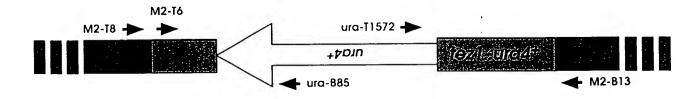


(These cells will show a senescence phenotype if the disrupted gene encodes a telomerase subunit.)

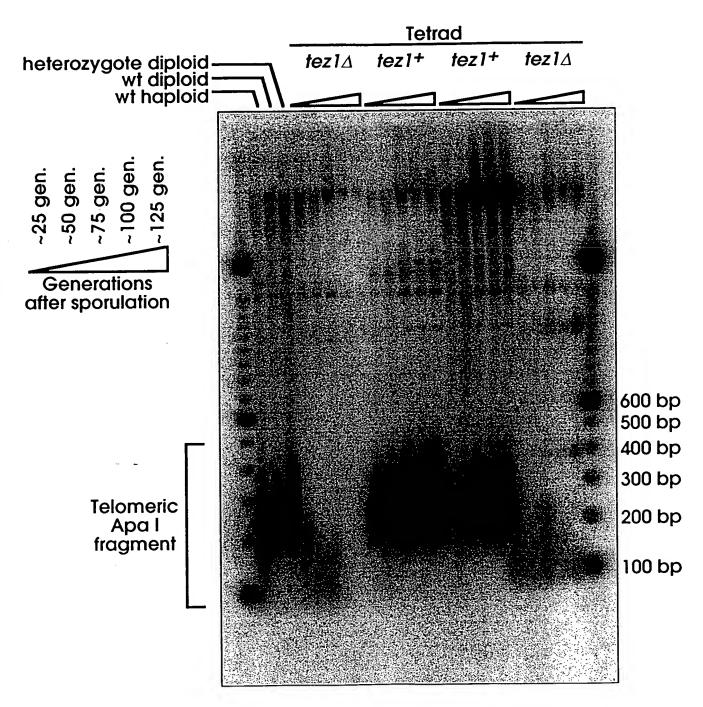
An Example of Confirmation of tez1 disruption By PCR







Tez1 disruption causes progressive shortening of telomeres in *S. pombe*



81 a 161 241 321 401 481 561 641 721 801 881	ctca ccaa ggtt agct ttaa gttg attg ccaa ataa gata acta	ataa gtat cgct ccttg acatg gagat aatat acttt attta	caat caagg tact ggagt ggagc attat catto cgtat cgcaa attta	acca acaa ttta agct cttg caaaa catc agct aaaaa	agtc aaag acaca caca cacat caaaa attt ctcgt attta	aaataacaatggt gaaa ttag tcatatattattag	tcca actt actg tcct atga gtcc ccac aggct aatt ccagt	atat cctt tttt taca gtca ttaca ttaca ttaca ctttt gata catt	gaag cccc agct aatc cgtc tggt actc tccg gtag atat	gtgt ctaa gcta ttct gcat ggta cttt tttt t	tatta agac cttc gatg gatg atcc aacg actc aaga aaaa	agtga tttta tagco agac gagta gega eetgg tttgg teet atat	atcga acttt caacc tatat atttga tttat aatcg tgat ataa agtt	ataat catta cgcgt ctaga ggtat cttt! gtace tctae tctae	actional control contr	actac actac actac actac actac actac actac actac actac actac	ttca cccg agtc gcaca tatt tatt atgtt atcaa	aata ytcat gcgtg gcct acgtc actca ccccc atatt	tegu tatt tgga taga tagt tctaa gttt	•	320 400 480 560 640 720
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1273 87		ATA I	GCG A	AAT N	GTT V	GTA V	AAA K	CAG Q	atg M	TTC F	GAT D	GAA E	AGT S	TTT F	GAG E	CGT R	CGA R	AGG R	AAT N	CTA L	1332 106
1333 107		ATG M	AAA K	GGG G	TTT F	TCC S	ATG M	gta	aggt	attc	taat	tgtga	aaat	attta	acct	gcaa	ttac	tgtt	tcaa	agaga	1405 113
1406 114	ttg	tatt	taac	cgata	aaag	AAT N	CAT H	GAA E	GAT D	TTT F	CGA R	GCC A	ATG M	CAT H	GTA V	AAC N	GGA G	GTA V	CAA Q	AAT N	1469 128
1470 129		CTC L	GTT V	TCT S	ACT T	TTT F	CCT P	AAT N	TAC Y	CTT L	ATA I	TCT S	ATA I	CTT L	GAG E	TCA S	AAA K	AAT N	TGG W	CAA Q	1529 148
1530 149		TTG L	TTA L	GAA E	AT q	gtaaa	ataco	ggt	taaga	atgt	tgcg	cacti	ttgaa	acaaq	gacto	gacaa	agta	tag '	r ato	G GGC	1601 155
1602 156	AGT S	GAT D	GCC A	ATG M	CAT H	TAC Y	TTA L	TTA L	TCC S	AAA K	GGA G	AGT S	ATT I	TTT F	GAG E	GCT A	CTT L	CCA P	AAT N	GAC D	1661 175
1662 176	AAT	TAC Y	CTT L	CAG Q	ATT I	TCT S	GGC G	ATA I	CCA P	CTT L	TTT F	AAA K	AAT N	AAT N	GTG V	TTT F	GAG E	GAA E	ACT T	GTG V	1721 195
1722 196		AAA K	AAA K	AGA R	AAG K	CGA R	ACC T	ATT I	GAA E	ACA T	TCC S	ATT I	ACT T	CAA Q	AAT N	AAA K	AGC S	GCC A	CGC R	AAA K	1781 215
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■ 216 ■ 4842 □ 907 □ 236 □ 1908	E AAG K TTA L CAA	V AAG K CAC H TTT	S TTT F TCT S	W AAG K ATT I CTT	N CAA Q TGT C ATA	S G gt D GAT D AAC	I caact CGG R	S aata AAC N TTT	I actgt ACA T CAA	S ctate GTA V GTG	R CCCC CAC H AAG	F cataa ATG M	S actaa TGG W TTG	I atttt CTT L CAC	F cag A CAA Q AAA	Y AT CT L TGG W	R TA TA Y ATT I	S AT TT F TTT F CCA	S TT AA N CCA P CTG	Y AC AGG R	2352451967
216 2842 1907 236 2908 246 1968	E AAG K TTA L CAA Q TCA	V AAG K CAC H TTT F	S TTT F TCT S GGA G	W AAG K ATT I CTT L ACA	N CAA Q TGT C ATA I	S G gt D GAT D AAC N	CGG R GCA A	S AAC N TTT F	I ACA T CAA Q CGT	S Etato GTA V GTG V	R CAC H AAG K	F Cataa ATG M CAA Q AAG	S TGG W TTG L GTA	I CTT L CAC H TAC	F CAA Q AAA K CCT	Y L TGG W GTG V	R Y ATT I ATT	S AT TT F CCA P	S TT AA N CCA P CTG L CAA	Y AC AGG R GTA V	235 245 1967 265 2027
216 2842 1907 236 2908 246 1968 266 2028	E AAG K TTA L CAA Q TCA S GCA	V AAG K CAC H TTT F CAG Q	S TTT F TCT S GGA G AGT S	W AAG K ATT I CTT L ACA T	N CAA Q TGT C ATA I GTT V	S G gt D GAT D AAC N GTG V	CGG R GCA A CCC P	AAC N TTT F AAA K	I ACA T CAA Q CGT R	S GTA V GTG V CTC L	CAC H AAG K CTA L	F Cataa ATG M CAA Q AAG K	S TGG W TTG L GTA V TAC	I CTT L CAC H TAC Y AAC	Eag ACAAQAAAAKCCTP	Y AT CT TGG W GTG V TTA L	R Y ATT I ATT I ATT I TGC	S AT TT F CCA P GAA E	S TT AA N CCA P CTG L CAA Q	Y AC AGG R GTA V ACA T	235 245 1967 265 2027 285 2087
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216 2842 2907 236 2908 246 1968 266 2028 286 2088 306 2148	E AAG K TTA L CAA Q TCA S GCA A GAC D TTT	V AAG K CAC H TTT F CAG Q AAG K ACC T	S TTT F TCT S GGA G AGT S CGA R CAC H	W AAG K ATT I CTT L ACA T CTC L GAT D	N CAA Q TGT C ATA I GTT V CAT H GAT D	G gt GAT D AAC N GTG V CGT R GAA E CTT	CGG R GCA A CCC P ATT I AAA K GTT	AAC N TTT F AAA K TCT S ATC I CGA	ACA T CAA Q CGT R CTA L CTT L	S GTA V GTG V CTC L TCA S AGT	CAC H AAG K CTA L AAA K TAT Y CCT	F cataa ATG M CAA Q AAG K GTT V TCC S	S TGG W TTG L GTA V TAC Y TTA	I CTT L CAC H TAC Y AAC N AAG K	Eag ACAAQAAAAKCCTPCATHCCCGPTGG	Y AT CT TGG W GTG V TTA L TAT Y AAC	R Y ATT I ATT I TGC C CAG Q AAC	S AT TT F TTT CCA P GAA E CCA P	S TT AA N CCA P CTG L CAA Q TAT Y TTT F AGG	Y AC AGG R GTA V ACA T ATT I GCG A	235 245 1967 265 2027 285 2087 305 2147 325 2207

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	2337 376				TTA L	TCG S	AGA R	TAC Y	GAG E	TCT S	TTT F	AGT S	TTA L	CAT H	TAT Y	TTA L	ATG M	AGT S	AAC N	ATA I	AAG K	2396 395
	2397 396	gtaa	tatg	ıccaa	attt	tttt	acca	ıttaa	ttaa	caat	cag	ATT I	TCA S	GAA E	ATT I	GAA E	TGG W	CTA L	GTC V	CTT L	GGA G	2465 405
	2466 406		AGG R	TCA S	AAT N	GCG A	AAA K	ATG M		TTA L	AGT S	GAT D	TTT F	GAG E	AAA K	CGC R	aag K	CAA Q	ATA I	TTT F	GCG A	2525 425
	2526 426	GAA	TTC F	ATC I	TAC Y	TGG W	CTA L		AAT N	TCG S	TTT F	ATA I	ATA I	CCT P	ATT I	TTA L	CAA Q	TCT S	TTT F	TTT F	TAT Y	2585 445
	2586 446	ATC				AGT S	GAT D	TTA L		AAT N	CGA R	ACT T	GTT V	TAT Y	TTT F	AGA R	AAA K	GAT D	ATT I	TGG W	AAA K	2645 465
	2646 466	СТС							ACA T	TCA S	ATG M	AAA K	ATG M	GAA E	GCG A	TTT F	GAA E	AAA ·	-ATA I	AAC N	GAG E	2705 485
	2706												C AAT	r gt	r ag	TA E	G GAT	r AC:	r cac	G AAJ K	A ACT	2775 495
0 0	486 2776								CGT R	CTA L	TTA L						TTT F		CTC L	ATT I	ACG T	2835 515
	496 2836		L TTA						АТА	AAG											tatta	
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	2968 543		TCG S	ATA I	CTG L	AAA K	CAT H	TTA L	ATC I	AAT N	GAA E	GAA E	AGT S	AGT S	GGT G	ATT I	CCA P	TTT F	AAC N	TTG L	GAG E	3027 562
	3028 563		TAC Y	ATG M	AAG K	CTT L	CTT L	ACT T	TTT F	AAG K	aag K	GAT D	CTT L	CTT L	AAG K	CAC H	CGA R	ATG M	TTT F	GG (gtaat	3088 581
	3089 582	tata	ataa	tgcg	cgati	tcct	catta	atta	attti	tgca		CGT A	AAG Z	AAG '	TAT Y	TTT(F	GTA (CGG /	ATA (GAT A	ATA I	3155 591
	3156 592		TCC S	TGT C	TAT Y	GAT D		ATA	AAG K	CAA Q	GAT D	TTG L	ATG M	TTT F	CGG R	ATT I	GTT V	AAA K	aag K	AAA K	CTC L	3215 611
	3216 612		GAT D	CCC P	GAA E	TTT F	GTA V	ATT I	CGA R	aag K	TAT Y	GCA A	ACC T	ATA I	CAT H	GCA A	ACA T	AGT S	GAC D	CGA R	GCT A	3275 631
	3276 632		AAA K	AAC N	TTT F	GTT V	AGT S	GAG E	GCG A	TTT F	TCC S	TAT Y	T g F	taag	ttta	tttt	ttca	ttgg	aatt	tttt	aacaa	3343 643
		att	cttt	ttta	g TT	GAT D	ATG M	GTG V	CCT P	TTT F	GAA E	AAA K	GTC V	GTG V	CAG Q	TTA L	CTT L	TCT S	ATG M	AAA K	ACA T	3405 659
		TCA	GAT D	ACT T	TTG L	TTT F	GTT V	GAT D	TTT F	GTG V	GAT D	TAT Y	TGG W	ACC T	AAA K	AGT S	TCT S	TCT S	GAA E	ATT I	TTT F	3465 679
		AAA						CTC L	TCT S	GGA G	CAC H	ATT I	GTT V	AAG K	gta	tacc	aatt	gttg	aatt	gtaa	taaca	3532 692

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	3533	ctaa	tgaa	acta	g AT	'A GO	AA AA	т то	T CA	A TA	C CI	T CA	A AA	A GI	T GO	ra Te	C CC	T CA	'C CC	C TC	CA C	3593
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					AAG K	K	G	S		L	L	R	V	V	D	D	F	L	F	I	Т	748
	729	r	1	r	V	K	G	5	v	_	_	• `	•	•	_							
	3714	СТТ	ААТ	AAA	AAG	GAT	GCA	AAA	AAA	TTT	TTG	AAT	TTA	тст	тта	AGA	G gt	gagt	tgct	gtca	ttcc	3777
	749		N		K	D	Α	K	K	F	L	N	L	S	L	R	G					764
	3778	taag	ttct	aacc	gttg	gaag	GA 7	TTT (GAG P						ACG A	AGC C	CTG C	GAG A	AAA A	ACA (STA -	3840
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	799		M	P	F	F	G	F	S	V	N	M	R	S	L	D	T	L	L	Α	С	818
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ñ	≟ ₫3961	ССТ	AAA	АТТ	GAT	GAA	GCC	TTA	TTT	AAC	TCT	ACA	TCT	GTA	GAG	CTG	ACG	AAA	CAT	ATG	GGG	4020
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		TGC	TGC	ААТ	АТА	TAT	AGG	СТА	GGA	TAC	тст	ATG	TGT	ATG	AGA	GCA	CAA	GCA	TAC	TTA	AAA	4209
Till Ham	869		С	N	I	Y	R	L	G	Y	S	М	С	M	R	Α	Q	Α	Y	L	K	888
ij	4210	AGG	ATG	AAG	GAT	ATA	TTT	ATT	CCC	CAA	AGA		TTC	ATA	ACG	G g	tgag	tacti	tatti	taad	ctaga	42/4
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	918			L	G	Y	T	S	R	R	F	L	S	S	Α	E	V	K	W			935
	4402	ggt	ctcga	agact	ttca	gcaa	tatt	gaca	catc	ag G	CTT	TTT	TGT	CTT	GGA	ATG	AGA	GAT	GGT	TTG	AAA	4468
	936										L	F	С	L	G	M	R	D	G	L	K	946
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	4469																TTT F	Q	S	L	T	966
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	967		L	I	AAG K		L	R		V		R	Q	V	L	F	L	Н	R	R	I	986
	-		-																			
	4589	GCT	GAT	TAA	tgt	catt	ttca	attt	atta	tata	catc	cttt	atta	ctgg	tgtc	ttaa	acaa	tatt	atta	ctaa	gtata	4665
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4746	gctgacccccaaagcaagcatactataggatttctagtaaagtaaaattaatctcgttattagttttgattga	4825
4906	$\verb atgcaaaaaagacgaagattatcttctaaacaagggggattaagcatatccgaaggaaaagagagtaatatacccagtgtt $	4985
	$\tt gttgaagaaagcaaggataatttggaacaagcttctgcagatgacaggctaaattttggtgaccgaattttggtaaaagc$	
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	tcctgatttaaaggaggaatcttccaccgatgaggaaatggatagcttatcagctgctgaggagaagcctaattttttgc	
	aaaaaagaaaatatcattgggagacatctcttgatgaatcagatgcggagagtatctccagcggatccttgatgtcaata	
		5544

GCCF	AGTT	CCTC	GCAC'I	'GGC'I	rg	1 met ATG	ser AGT	val GTG	tyr TAC	val GTC	val GTC	glu GAG	leu CTG	leu CTC
10 arg	ser TCT	phe TTC	phe TTT	tyr TAT	val GTC	thr ACG	glu GAG	thr ACC	thr ACG	20 phe TTT	gln CAA	lys AAG	asn AAC	arg AGG
leu	phe	phe	tyr	arg	30 lys	ser	val	trp	ser	lys	leu	gln CAA	ser	ile
40 alv	ile	arg	gln	his	leu	lys	arq	val	gln	50 leu	arg	glu GAG	leu	 ser
qlu	ala	glu	val	arq	60 gln	his	arg	glu	ala	arg	pro	ala GCC	leu	leu
70 thr	ser	arg	leu	arg	phe	ile	pro	lys	pro	80 asp	gly	leu CTG	arg	pro
ile	val	asn	met	asp	90 tyr	val	val	gly	ala	arg	thr	phe	arg	arg
100 glu	lvs		ala	qlu	arq	leu	thr	ser	arg	110 val	lys	TTC	leu	phe
ser	val ["]	leu	asn	tyr'	120 glu	arq	ala	arg	arg	pro	gly	GCA leu	leu	gly
130										140		CTC		thr
GCC	TCT	GTG	CTG	GGC	CTG 150	GAC	GAT	ATC	CAC	AGG	GCC	TGG	CGC	ACC
TTC 160	GTG	CTG	CGT	GTG	CGG	GCC	CAG	GAC	CCG	CCG 170	CCT	GAG	CTG	tyr TAC
TTT	GTC	AAG	GTG	GAT	GTG 180	ACG	GGC	GCG	TAC	GAC	ACC	ATC	ccc	gln CAG
asp GAC	arg AGG	leu CTC	thr ACG	glu GAG	val GTC	ile ATC	ala GCC	ser AGC	ile ATC	ile ATC	lys AAA	pro CCC	gln CAG	asn AAC

t	190 hr ACG	tyr TAC	cys TGC	val GTG	arg CGT	arg CGG	tyr TAT	ala GCC	val GTG	val GTC	200 gln CAG	lys AAG	ala GCC	ala GCC	met ATG
Ç	gly GGC	thr ACG	ser TCC	ala GCA	arg AGG	210 pro CCT	ser TCA	arg AGA	ala GCC	thr ACG	ser TCC	tyr TAC	val GTC	gln CAG	cys TGC
C	220 gln CAG	gly GGG	ile ATC	pro CCG	gln CAG	gly GGC	ser TCC	ile ATC	leu CTC	ser TCC	230 thr ACG	leu CTG	leu CTC	cys TGC	ser AGC
	leu CTG	cys TGC	tyr TAC	gly GGC	asp GAC	240 met ATG	glu GAG	asn AAC	lys AAG	leu CTG	phe TTT	ala GCG	gly GGG	ile ATT	arg CGG
ć	250 arg CGG	asp GAC	gly GGG	leu CTG	leu CTC	leu CTG	arg CGT	leu TTG	val GTG	asp GAT	260 asp GAT	phe TTC	leu TTG	leu TTG	val GTG
t Z	thr ACA	pro CCT	his CAC	leu CTC	thr ACC	270 his CAC	ala GCG	lys AAA	thr ACC	phe TTC	leu CTC	arg AGG	thr ACC	leu CTG	val GTC
ä	280 arg CGA	gly GGT	val GTC	pro CCT	glu GAG	tyr TAT	gly GGC	cys TGC	val GTG	val GTG	290 asn AAC	leu TTG	arg CGG	lys AAG	thr ACA
7	val GTG	val GTG	asn AAC	phe TTC	pro CCT	300 val GTA	glu GAA	asp GAC	glu GAG	ala GCC	leu CTG	gly GGT	gly GGC	thr ACG	ala GCT
1	310 ohe TTT	val GTT	gln CAG	met ATG	pro CCG	ala GCC	his CAC	gly GGC	leu CTA	phe TTC	320 pro CCC	trp TGG	cys TGC	gly GGC	leu CTG
	leu CTG	leu CTG	asp GAT	thr ACC	arg CGG	330 thr ACC	leu CTG	glu GAG	val GTG	gln CAG	ser AGC	asp GAC	tyr TAC	ser TCC	ser AGC
1	340 tyr TAT	ala GCC	arg CGG	thr ACC	ser TCC	ile ATC	arg AGA	ala GCC	ser AGT	leu CTC	350 thr ACC	phe TTC	asn AAC	arg CGC	gly GGC
]	phe TTC	lys AAG	ala GCT	gly GGG	arg AGG	360 asn AAC	met ATG	arg CGT	arg CGC	lys AAA	leu CTC	phe TTT	gly GGG	val GTC	leu TTG
	370 arg	leu	lvs	CVS	his	ser	leu	phe	leu	asp	380 leu	qln	val	asn	ser AGC



leu gln thr										
400 ala tyr arg GCG TAC AGG										
gln val trp CAA GTT TGG										
430 arg leu pro CGG CTC CCT										
val ala gly GTC GCT GGG	gly gln GGC CAA	450 gly ar GGG CC	g arg GC CGC	arg CGG	pro CCC	ser TCT	ala GCC	leu CTC	arg CGA	gly GGC
460 arg ala val CGT GCA GTG										
thr pro cys ACA CCG TGT	his leu CAC CTA	480 arg al	a thr CC ACT	pro CCT	gly GGG	val GTC	thr ACT	gln CAG	asp GAC	ser AGC
490 pro asp ala CCA GAC GCA	ala glu GCT GAG	ser gl TCG GA	u ala A GCT	pro CCC	gly GGG	500 asp GAC	asp GAC	ala GCT	asp GAC	cys TGC
pro gly gly CCT GGA GGC	arg ser CGC A GC	510 gln pr CAA CO	o gly	thr ACT	ala GCC	leu CTC	arg AGA	leu CTT	gln CAA	asp GAC
520 his pro gly CAT CCT GGA	leu met CTG ATG	ala th	r arg	pro CCA	gln CAG	530 pro CCA	gly GGC	arg CGA	glu GAG	gln CAG
thr pro ala ACA CCA GCA	ala leu GCC CTG	540 ser an TCA CO	g arg GC CGG	ala GCT	tyr TAT	thr ACG	ser TCC	gln CAG	gly GGA	gly GGG
550 arg gly gly AGG GGC GGC	pro his CCA CAC	pro gl	y leu GC CTG	his CAC	arg CGC	560 trp TGG	glu GAG	ser TCT	glu GAG	ala GCC
564 OP TGA GTGAGTG	TTTGGCCG	AGGCCT(GCATGT	CCGG(CTGA	AGGC'	rgag'	rgtc(CGGC'	rgaggc
CTGAGCGAGTG	TCCAGCCA	AGGGCT(SAGTGT	CCAG	CACA	CCTG	CGTT	rtca(CTTC	CCCAC







Motif -1 Ep p123 Sp Tez1 Sc Est2 Hs TCP1 consensus	LVVSLIRCFFYVTEQQKSYSKTFIIPILQSFFYITESSDLRNRTLIPKIIQTFFYCTEISSTVTIVYVVELLRSFFYVTETTFQKNRL FFY TE
Motif 0 Ep p123 Sp Tez1 Sc Est2 Hs TCP1 consensus	K phhh K hR h RKSLGFAPGKLRLIPKKTTFRPIMTFNKKIVQKTTLPPAVIRLLPKKNTFRLITNLRKRFLTLSNFNHSKMRIIPKKSNNEFRIIAIPCRGADARPALLTSRLRFIPKPDGLRPIVNMDYVVG R PK R I
Motif A Ep p123 Sp Tez1 Sc Est2 Hs TCP1 consensus	AF h hDh GY hPKLFFATMDIEKCYDSVNREKLSTFLKRKKYFVRIDIKSCYDRIKQDLMFRIVKPELYFMKFDVKSCYDSIPRMECMRILKPELYFVKVDVTGAYDTIPQDRLTEVIA// F D YD
Motif B Ep p123 Sp Tez1 Sc Est2 Hs TCP1 consensus	hPQG pS hhNGKFYKQTKGIPQGLCVSSILSSFYYAGNSQYLQKVGIPQGSILSSFLCHFYMEEDKCYIREDGLFQGSSLSAPIVDLVYDRATSYVQCQGIPQGSILSTLLCSLCYG G QG S
Motif C Ep p123	Y h F DDhhh PNVNLLMRLTDDYLLITTQENN
Sp Tez1 Sc Est2 Hs TCP1 consensus	KKGSVLLRVVDDFLFITVNKKD SQDTLILKLADDFLIISTDQQQ RRDGLLLRLVDDFLLVTPHLTH DD L
Motif D Ep p123 Sp Tez1 Sc Est2 Hs TCP1 consensus	Gh h cKNVSRENGFKFNMKKLLNLSLRGFEKHNFSTKKLAMGGFQKYNAKALRTLVRGVPEYGCVV G